In response to the Notice to Comply, Applicants submit herewith the required paper copy and computer readable copy of the Sequence Listing. Please amend the specification in adherence with 37 C.F.R. §§ 1.821-1.825 as follows.

In the Specification:

Please replace the paragraph beginning at page 1, line 22, with the following:

A1

--PDZ domains of proteins are named after three prototypical proteins: PSD95, Drosophila large disc protein and Zonula Occludin 1 protein (Gomperts et al., 1996, *Cell* 84:659-662). PDZ domain-containing proteins are involved in synapse formation by organizing transmembrane neurotransmitter receptors through intracellular interactions. PDZ domains contain the signature sequence GLGF (SEQ ID NO:29). In the nervous system, typical PDZ domain-containing proteins contain three PDZ domains, one SH3 domain and one guanylate kinase domain. Examples of intracellular PDZ domain-containing proteins include LIN-2, LIN-7 and LIN-10 at the pre-synapse, and PSD95 at the post-synapse.--

Please replace the paragraph beginning at page 12, line 1, with the following:

A2

--5.3 As used herein, the term "PDZ domain" refers to protein sequence (i.e., modular protein domain) of approximately 90 amino acids, characterized by homology to the brain synaptic protein PSD-95, the Drosophila septate junction protein Discs-Large (DLG), and the epithelial tight junction protein ZO1 (ZO1). PDZ domains are also known as Discs-Large homology repeats ("DHRs") and GLGF (SEQ ID NO:29) repeats). PDZ domains generally appear to maintain a core consensus sequence (Doyle, D. A., 1996, Cell 85: 1067-1076).--

A3

Please replace the paragraph (TABLE 2) beginning at page 26, line 1, with the following (see attached sheets).

PDZ-LIGAND/PDZ INTERACTION SUMMARY

TABLE 2

PDZ LIGAND	CODE	SEQ	SEQ ID NO:	CASK	MPP1	DLG1	PSD95	NeDLG	TAX33	SYN1a	TAX 43	LDP	LIM	LIMK1	LIMK2	MPP2
CD6	AA6L	ISAA	14													
CD49E (alpha-4)	AA11L	TSDA	24													
CD49F (Aform. alpha6)	AA12L	TSDA	24													
CD166 (CD6L)	AA20L	KTEA	64													
CD148	AA55L	KTIA	278													
CC CKR-2	AA42L	KEGA	283													
CD138 (syndecan)	AA18L	EFYA	89	*												
CD148 (DEP-1)	AA19L	GYIA	119													
CD98 (2F4)	AA15L	PYAA	54													G
CLASP-1	AA1L	SAEV	284			G	A	G								
CLASP-4	AA3L-V	YAEV	228			A	A	A				A				
NMDA	AA34.2L	ESDV	263		A	A/G	A/G	A/G		G	A			A		G
VCAM1	AA17L	KSKV	163		A	A		A				A				
CLASP-2	AA2L	SSVV	223			A/G	A/G	A/G								
CD95 (Apo-1/Fas)	AA13L	QSLV	44			A/G	A/G	A/G								
KV1.3	AA33L	FTDV	238			A/G*	A/G*	A/G						A		
DNAM-1	AA22L	KTRV	74		A	A	A/G	A					A			G
CD83	AA47L	TELV	248			A	A	A								
CD44 (long form)	AA3L	KIGV	104		G											
Neurexin	AA38L	EYYV	268	G*	A*	A/G	A/G	G		A	A			A		
CD97 (CD55L)	AA14L	ESGI	49			A										
Glycophorin C	AA37L	EYFI	273		*	G	G	G								A
CDW128A (IL8RA)	AA29.1L	SSNL	69			A		A								
CD3n	AA4L	SSQL	4			A	A									
LPAP	AA30L	VTAL	84			A										
CD46 (form 1)	AA10L	FTSL	109			A/G	A/G	G								
CDW128B (IL8RB)	AA29.2L	STTL	233			A/G	A	A/G								
DOCK2	AA40L	STDL	243			A	A/G	G		G						
CD34	AA7L	DTEL	149			A	A	G								
CD5	AA49L	AQRL	285													
CC CKR-4	AA44L	HDAL	286													
FceRIb	AA25L	PIDL	129													
FasLigand	AA23L-M	LYKL	79													
CD62E	AA48L	SYIL	168													
CC CKR-1R	AA41L	SAGF	287													
CDW125 (IL5R)	AA28L	DSVF	94													
BLR-1	AA45L	LTTF	253													
CC CKR-3	AA43L	SIVF	288													
				CASK	MPP1	DLG1	PSD95	NeDLG	TX33	SYN1a	TX 43	LDP	LIM	LIMK	LIMK2	MPP2

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* Interactions described in the scientific literature

PDZ-LIGAND/PDZ INTERACTION SUMMARY

TABLE 2
CONTINUED

NOS1	AF6	PTN-4	prIL16	41.8	K559	RGS12	K316	DVL1	TAX 40	TIAM1	MINT1	K303	CBP	MINT3	TAX 2	K561	PDZ LIGAND
				A													CD6
				A/G													CD49E (alpha-4)
				A/G													CD49F (Aform, alpha6)
																	CD166 (CD6L)
																	CD148
																	CC CKR-2
				A/G						A							CD138 (syndecan)
																	CD148 (DEP-1)
																	CD98 (2F4)
																	CLASP-1
	A			A							A						CLASP-4
		A/G		A/G		A/G		A			A/G				A	G	NMDA
				A						A		A					VCAM1
				A													CLASP-2
				A/G													CD95 (Apo-1/Fas)
				A		A		A			G						KV1.3
	A			A		A											DNAM-1
																	CD83
			G								G						CD44 (long form)
	A		A	A		A		A	A	A	A/G						Neurexin
				A													CD97 (CD55L)
	A			A							A						Glycophorin C
																	CDW128A (IL8RA)
				A/G							A/G						CD3n
											G						LPAP
																	CD46 (form 1)
				A		*											CDW128B (IL8RB)
																G	DOCK2
																	CD34
																	CD5
																	CC CKR-4
											A						FceRIb
																G	FasLigand
																	CD62E
																	CC CKR-1R
		G				G											CDW125 (IL5R)
											G						BLR-1
																	CC CKR-3
NOS1	AF6	PTN-4	prIL16	41.8	K559	RSG12	K316	DVL1	TX 40	TIAM1	MINT1	K303	CBP	MINT3	TX 2	K561	

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* Interactions described in the scientific literature

A4 Please replace the paragraph (TABLE 3) beginning at page 33, line 1, with the following (see attached sheets).

Please replace the paragraph beginning at page 50, line 25, with the following:

--As noted *supra*, PCR primers were designed to include endonuclease restriction sites to facilitate ligation of PCR fragments into a GST gene fusion vector (pGEX-3X; Pharmacia, GenBank accession no. XXU13852) in-frame with the glutathione-S transferase coding sequence. This vector contains a IPTG inducible lacZ promoter. The pGEX-3X vector was linearized using *Bam* HI and *Eco* RI or, in some cases, *Eco* RI or *Sma* I, as shown in **TABLE 3**, and dephosphorylated. For most cloning approaches, double digest with Bam HI and Eco RI was performed, so that the ends of the PCR fragments to clone were Bam HI and Eco RI. In some cases, restriction endonuclease combinations used were Bgl II and Eco RI, Bam HI and Mfe I, or Eco RI only, Sma I only, or BamHI only (see **TABLE 3**).

A5 When more than one PDZ domain was cloned, the DNA portion cloned represents the PDZ domains and the cDNA portion located between individual domains. Precise locations of cloned fragments used in the assays are indicated in **TABLE 3**. DNA linker sequences between the GST portion and the PDZ domain containing DNA portion vary slightly, dependent on which of the above described cloning sites and approaches were used. As a consequence, the amino acid sequence of the GST-PDZ fusion protein varies in the linker region between GST and PDZ domain. Protein linkers sequences corresponding to different cloning sites/approaches are shown below. Linker sequences (vector DNA encoded) are bold, PDZ domain containing gene derived sequences are in italics.

1) **GST—BamHI**/*BamHI— PDZ domain insert*
Gly--Ile—*PDZ domain insert*

2) **GST—BamHI**/*BglII—PDZ domain insert*
Gly—Ile—*PDZ domain insert*

3) **GST—EcoRI**/*EcoI—PDZ domain insert*
Gly—Ile—Pro—Gly--Asn—*PDZ domain insert* (SEQ ID NO:258)

4) **GST--SmaI**/*SmaI—PDZ domain insert*
Gly—Ile—Pro—*PDZ domain insert--*

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TABLE 3
PDZ DOMAINS

Key:

Gene names and corresponding gene products are provided. In some cases, cDNA sequences representing the same gene have several database entries under different accession numbers and names. Accession numbers shown correspond to the gene name used in this description, and numbering of nucleotides and amino acids correlates to those Genbank entries. Amino acid sequences shown correspond to the cloned DNA portions of PDZ domain containing genes. Linker amino acid sequences (e.g., amino acids encoded by DNA flanking the cloning site of the pGEX-3X cloning vector) are in italics

GENE SYMBOL	PROTEIN	ACC.#	AMINO ACID SEQUENCE*	CLON. SITES	FORWARD PRIMER	REVERSE PRIMER
CASK	CASK	Y17138	AA495-584; PDZ domain 1 (of 1) *HV*TRVRLVQFQKNTDEPMGITLK MNELNHCIVARIMHGGMIHRQGT LHVGDEIREINGISVANQTVEQL QKMLREMRGSITFKIVPSYRTQS *LNSS* (SEQ ID NO:292)	Bam HI / Eco RI	6CAF 5'- TCGGATCCAT GTGACCAGAG TTCGG-3' (SEQ ID NO:322) N1471-1494	7CAR 5'- TCGGAATTCAG ACTGAGTGCGG TA-3' (SEQ ID NO:323) N1761-1738

MPP1	55 Kd erythrocyte membrane protein	M64925	AA101-186; PDZ domain 1 (of 1) RKVRLIQFEKVTEEPMGITLKLN EKQSCTVARILHGGMIHRQGSLH VGDEILEINGTNVTNHSVDQLQK AMKETKGMISLKVIPNQ*REFIVT D* (SEQ ID NO:293)	Bam HI / Bam HI	62MPF 5'-GGGATCCGGA AAGTGCGACT CATAC-3' (SEQ ID NO:324) N296-320	63MPR 5'-ACGGATCCGCT GGTTGGGAATT ACTT-3' (SEQ ID NO:325) N568-543
DLG1	human homolog of Drosophila discs large protein	U13897	AA275-477; PDZ domains 1-2 (of 3) *Q*VNGTDADYEYEEITLERGNSGL GFSIAGGTDNPHIGDDSSIFITK IITGGAAAQDGRLRVNDCILQVN EVDVRDVTHSKAVEALKEAGSIV RLYVKRRKPVSEKIMEIKLIKGP KGLGFSIAGGVGNQHIPGDNSIY VTKIIEGGAAHKDGKLQIGDKLL AVNNVCLEEVTHEEAVTALKNTS DFVYLKVAKPTSMYMNDGYA*PNS S* (SEQ ID NO:294)	Bam HI / Eco RI	1DF 5'-TCGGATCCAG GTTAATGGCT CAGATG-3' (SEQ ID NO:326) N815-841	2DR 5'-CGGAATTCGGT GCATAGCCATC -3' (SEQ ID NO:327) N1442-1421

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PSD95	human post-synaptic density protein 95	U83192	AA387-724; PDZ domains 1-3 (of 3) *LEG*EGEMEYEEITLERGNSGLGF SIAGGTDNPHIGDDPSIFITKII PGGAAAQDGRLRVNDSILFVNEV DVREVTHSAAVEALKEAGSIVRL YVMRRKPPAEKVMEIKLIKGPKG LGFSIAGGVGNQHIPGDNSIYVT KIIEGGAAHKDGRLQIGDKILAV NSVGLEDVMHEDAVAALKNTYDV VYLKVAKPSNAYLSDSYAPPDIT TSYSQHLDNEISHSSYLGTDYPT AMTPTSPRRYSPVAKDLLGEEDI PREPRRIVIHRGSTGLGFNIVGG EDGEGIFISFILAGGPADLSGEL RKGDQILSVNGVDLRNASHEQAA IALKNAGQTVTIIAQYKPE*FIV* (SEQ ID NO:295)	Bam HI / Eco RI	8PSF 5'- TCGGATCCTT GAGGGGGAGA TGGA-3' (SEQ ID NO:328) N1150-1173	11PSR 5'- TCGGAATTCGC TATACTCTTCT GG-3' (SEQ ID NO:329) N2191-2168

NeDLG	presynaptic protein sao102 (neuroendo-crine-dlg)	U49089	AA205-1171; PDZ domains 1-2 (of 3) *Q*YEEIVLERGNSGLGFSIAGGID NPHVPDDPGIFITKIIPGGAAAM DGRLGVNDCVLRVNEVEVSEVVH SRAVEALKEAGPVVRLVVRRRQP PPETIMEVNLLKGPKGLGFSIAG GIGNQHIPGDNSIYITKIIEGGA AQKDGRLQIGDRLLAVNNTNLQD VRHEEAVASLKNTSDMVYLKVAK PGS*PR* (SEQ ID NO:296)	Bam HI / Eco RI	71NEDF 5'- CAGGATCCAA TATGAGGAAA TCGTACTTG- 3' (SEQ ID NO:330) N608-635	72NEDR 5'- TTGAATTCGAG GCTGCCTGGCT TGGC-3' (SEQ ID NO:331) N1186-1161
TAX33	tax interaction protein 33	AF028826	AA73-162; PDZ domain 1 (of 1) HSHPRVVELPKTDEGLGFNVMGG KEQNSPIYISRIIPGGVAERHGG LKRGDQLLSVNGVSVEGEHHEKA VELLKAAKDSVKLVVRYTPKVL*E* *FIVTN* (SEQ ID NO:297)	Bam HI / Eco RI	92TAF 5'- GTGGGATCCA CTCCCACCCT CGAGTAG-3' (SEQ ID NO:332) N208-234	93TAR 5'- CATGAATTCCA GAACTTTTGGG TGTATCGC-3' (SEQ ID NO:333) N497-468

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SYN 1 α	alpha1-syntrophin	U40571	AA96-189 PDZ domain 1 (of 1) QRRRVTVRKADAGGLGISIKGGR ENKMPILISKIFKGLAADQTEAL FVGDAILSVNGEDLSSATHDEAV QVLKKTGKEVVLEVKYMKDVSPY FK*NSS* (SEQ ID NO:298)	Bam HI / Eco RI	124SYF 5'- TACGGATCCA GCGGCCGCCG CGTGAC-3' (SEQ ID NO:334) N279-301	125SYR 5'- GTAGAATTCTT GAAATACGGTG AGAC-3' (SEQ ID NO:335) N576-551

TAX43	human tax interaction protein 43	AF028828	AA15-85 PDZ domain 1 (of 1) QKRGVKVLKQELGGLGISIKGGK ENKMPILISKIFKGLAADQTQAL YVGDAILSVNGADLRDATHDEAV QAL*QFIVTN* (SEQ ID NO:299)	Bam HI / Eco RI	97TAF 5'- TCTGGATCCA GAAGCGTGGC GTGAAGG-3' (SEQ ID NO:336) N37-63	98TAR 5'- CGGAATTCAAC GCCTGCACCGC CTC-3' (SEQ ID NO:337) N267-231

LDP	lim domain protein clp-36	U90878	AA46-88 PDZ domain 1 (of 1) RGMTTQQIDLQGPGPWGFRLVGR KDFEQPLAISRVTPGSKAALA*SS* (SEQ ID NO:300)	Bam HI / Eco RI	146LIF 5'- CCAGGATCCG CGGAATGACC ACCCAGC-3' (SEQ ID NO:338) N129-155	147LIR 5'- CATGAATTCGC TAGAGCCGCCT TGCTT-3' (SEQ ID NO:339) N276-239

LIM	Human LIM protein	AF061258	AA29-112; PDZ domain 1 (of 1) *LS*NYSVSLVGPAPWGFRLQGGKD FNMPLTISSLKDGGKAAQANVRI GDVVLSIDGINAQGMTHLEAQNK IKGCTGSLNMTLQRAS*C* (SEQ ID NO:301)	Bam HI / Eco RI	182LF 5'- TTAGGATCCT GAGCAAGTAC AGTGTGTCAC -3' (SEQ ID NO:340) N86-115	183LR 5'- CTTGAATTCAG CAGATGCTCTT TGCAGAGTC- 3' (SEQ ID NO:341) N350-320
LIMK1	human LIM domain kinase 1	NM_ 002314	AA194-291; PDZ domain 1 (of 1) *T*VTLVSIPASSHGKRGLSVSIDP PHGPPGCGTEHSHTVRVQGVDPG CMSPDVKNSIHVGDRILEINGTP IRNVPLDEIDLLIQETSRLLQLT LEHD*PGIHRD* (SEQ ID NO:302)	SMA I	52LIFP 5'- CTGCCCGGGA CCGTCACCCT GGTGTCC-3' (SEQ ID NO:342) N570-597	53LIRP 5'- TCGCCCGGGTC ATGCTCGAGGG TC-3' (SEQ ID NO:343) N874-851

LIMK2	human LIM domain kinase 2	D45906	AA185-275; PDZ domain 1 (of 1) PYSVTLISMPATTEGRRGFSVSV ESACSNYATTVQVKEVNRMHISP NNRNAIHPGDRILEINGTPVRTL RVEEVEDAISQTSQTLQLLIEH*E FIVTN* (SEQ ID NO:303)	Bam HI / Eco RI	185LF 5'-AGCGGATCCC CTACTCTGTC ACGCTCATC-3' (SEQ ID NO:344) N545-573	186LR 5'-GACGAATTCAT GTTCAATCAAC AGCTGAAG-3' (SEQ ID NO:345) N834-805
MPP2	maguk p55 subfamily member 2 (DLG2)	X82895	AA185-273; PDZ domain 1 (of 1) *Q*PVPPDAVRMVGIRKTAGEHLGV TFRVEGGELVIARILHGGMVAQQ GLLHVGDIIKEVNGQPVGSDPRA LQELLRNASGSVILKILPNYQ*VF IVTD* (SEQ ID NO:304)	Bam HI / Eco RI	142MF 5'-TCAGGATCCA GCCTGTACCT CCCGATGC-3' (SEQ ID NO:346) N542-569	143MR 5'-ATGGAATTCCT GGTAGTTGGGC AGGATC-3' (SEQ ID NO:347) N828-801

NOS1	human neuronal nitric oxide synthase	U17327	AA239-988; PDZ domain 1 (of 1) IQPNVISVRLFKRKVGGLGFLVK ERVSKPPVIISDLIRGGAAEQSG LIQAGDIILAVNGRPLVDLSYDS ALEVLRGIASETHVVLILRGP*EF IVTD* (SEQ ID NO:305)	Bam HI / Eco RI	155NOF 5′-AGCGGATCCA GCCCAATGTC ATTTC-3′ (SEQ ID NO:348) N711-733	156NOR 5′-GAAGAATTCAG GGCCCCTCAGA ATG-3′ (SEQ ID NO:349) N994-970
AF6	af-6 protein	U02478	AA985-1077; PDZ domain 1 (of 1) LRKEPEIITVTLKKQNGMGLSIV AAKGAGQDKLGIYVKSVVKGGAA DVDGRLAAGDQLLSVDGRSLVGL SQERAAELMTRTSSVVTLEVAKQ *GEFIVTD* (SEQ ID NO:306)	Bam HI / Eco RI	66AFF 5′-TCGGATCCTG AGGAAAGAAC CTGAA-3′ (SEQ ID NO:350) N2946-2970	67AFR 5′-TAGAATTCACC CTGCTTTGCTA CTTC-3′ (SEQ ID NO:351) N3239-3214

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PTN-4	protein-tyrosine phosphatase meg1	M68941	AA774-862; PDZ domain 1 (of 1) LIRMKPDENGRFGFNVKGGYDQK MPVIVSRVAPGTPADLCVPRLNE GDQVVLINGRDIAEHTHDQVVLF IKASCERHSGELMLLVRPNA*EFI VTD* (SEQ ID NO:307)	Bam HI / Eco RI	247PTF 5'-ATCGGATCCT AATCAGAATG AAACCTG-3' (SEQ ID NO:352) N2312-2338	248PTR 5'-ATCGAATTCAG CATTAGGTCGA ACTAG-3' (SEQ ID NO:353) N2595-2569
prIL16	putative interleukin 16 precursor	S81601	AA170-383; PDZ domain 1-2 (of 2) HVTILHKEEGAGLGFSLAGGADL ENKVITVHRVFPNGLASQEGTIQ KGNEVLSINGKSLKGTTHHDALA ILRQAREPRQAVIVTRKLTPEAM PDLNSSTDSAASASAASDVSVES TAEATVCTVTLEKMSAGLGFSLE GGKGSLHGDKPLTINRIFKGAAS EQSETVQPGDEILQLGGTAMQGL TRFEAWNIIKALPDGPVTIVIRR KSLQSK*EFIVTD* (SEQ ID NO:308)	Bam HI / Eco RI	75PRF 5'-ACGGGATCCA TGTCACCATC TTACAC-3' (SEQ ID NO:354) N503-528	76PRR 5'-GTGAATTCCTT GGACTGGAGGC TTTTTC-3' (SEQ ID NO:355) N1157-1129

41.8 kD	hypothetical 41.8 kD protein	AF007156	AA4-85; PDZ domain 1 (of 1) RDSGAMLGLKVVGGKMTESGRLC AFITKVKKGSLADTVGHLRPGDE VLEWNGRLLQGATFEEVYNIILE SKPEPQVELVVSR*ANSS* (SEQ ID NO:309)	Bam HI / Eco RI	145HF 5'-GTGGGATCCG AGATTCAGGA GCAATGC-3' (SEQ ID NO:356) N4-30	146HR 5'-CTGGAATTCGC CTTGAAACTAC AAGTTC-3' (SEQ ID NO:357) N267-240
K559	KIAA0559	AB011131	AA766-870; PDZ1 (of 1) HYIFPHARIKITRDSKDHTVSGN GLGIRIVGGKEIPGHSGEIGAYI AKILPGGSAEQTGKLMEGMQVLE WNGIPLTSKTYEEVQSIISQQSG EAEICVRLDLNML*SNSS* (SEQ ID NO:310)	Bam HI / Eco RI	130KIF 5'-AAAGGATCCA CTACATCTTT CCTCACG-3' (SEQ ID NO:358) N2290-2312	131KIR 5'-TCACAATTGGA TAGCATATTGA GGTCCAG-3' (SEQ ID NO:359) N2623-2595
RGS12	human regulator of G-protein signalling 12	AF035152	AA35-103; PDZ domain 1 (of 1) *PPPRVRSVEVARGRAGYGFTLSG* QAPCVLSCVMRGSPADFVGLRAG DQILAVNEINVKKASHEDVVKLI *GNSS* (SEQ ID NO:311)	Bam HI / Eco RI	64RGF 5'-TGGGATCCCG CCCCCAAGGG TGCGGAG-3' (SEQ ID NO:360) N93-119	65RGR 5'-AGGAATTCCCA ATTAATTTCAC TAC-3' (SEQ ID NO:361) N316-291

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K316	KIAA0316	AB002314	AA197-284; PDZ domain 1 (of 1) PPAPRKVEMRRDPVLGFGFVAGS EKPVVVRSVTPGGPSEGKLIPGD QIVMINDEPVSAAPRERVIDLVR SCKESILLTVIQPYPSPK*RNSS* (SEQ ID NO:312)	Bam HI / Eco RI	158KIF 5'- AAAGGATCCC TCCGGCTCCT CGGAAG-3' (SEQ ID NO:362) N586-611	159KIR 5'- TTAGAATTCTG ATTTGGGAGAA GGGTAAG-3' (SEQ ID NO:363) N866-839

DVL1	human dishevelled segment polarity protein homolog	AF006011	AA248-340; PDZ domain 1 (of 1) *QSTV*LNIVTVTLNMERHHFLGIS IVGQSNDRGDGGIYIGSIMKGGA VAADGRIEPGDMLLQVNDVNFEN MSNDDAVRVLREIVSQTGPISLT VAKC*WEFIVTD* (SEQ ID NO:313)	Bam HI / Eco RI	1st PCR: 55DVISF 5'-TCATCCAGAC TCATCCGGAA G-3' (SEQ ID NO:364) N652-673 2nd PCR, nested: 37DVF 5'-TCGGATCCAA ACGGTCACTC TCAAC-3' (SEQ ID NO:366) N723-747	1stPCR: 56DVISR 5'-GCTCATGTCAC TCTTCACCG-3' (SEQ ID NO:365) N1195-1174 2nd PCR, nested: 38DVR 5'-TCGGAATTCCC AGCACTTGGCT ACAG-3' (SEQ ID NO:367) N1029-N1004

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TAX40	human tax interaction protein 40	AF028827	AA35-137; PDZ domain 1 (of 1) LLPETHRRVRLHKHGSDRPLGFY IRDGMSVRVAPQGLERVPGIFIS RLVRGGLAESTGLLAVSDEILEV NGIEVAGKTLDQVTDMMVANSHN LIVTVKPANQ*ANSS* (SEQ ID NO:314)	Bam HI / Eco RI	136TF 5′- ACGGGATCCT ACTGCCTGAG ACCCACC-3′ (SEQ ID NO:368) N97-123	137TR 5′- ACGGAATTCCG CTGGTTGGCGG GCTTGAC-3′ (SEQ ID NO:369) N421-393
TIAM1	T- lymphoma invasion and metastasis inducing protein 1	NM_ 003253	AA1001-1088; PDZ 1 (of 1) HSIHIEKSDTAADTYGFSLSSVE EDGIRRLYVNSVKETGLASKKGL KAGDEILEINNRAADALNSSMLK DFLSQPSLGLLVRTYPELE*EFIV TD* (SEQ ID NO:315)	Bam HI / Eco RI	39TF 5′- TCGGATCCAC AGCATCCACA TTGAG-3′ (SEQ ID NO:370) N2995-3019	40TR 5′- TCGGAATTCCT CCAGCTCGGGG T-3′ (SEQ ID NO:371) N3275-3253

MINT1	human X11 protein	L04953	AA717-894; PDZ domains 1-2 (of 2) SENCKDVFIEKQKGEILGVVIVE SGWGSILPTVIIANMMHGGPAEK SGKLNIGDQIMSINGTSLVGLPL STCQSIIKGLENQSRVKLNIVRC PPVTTVLIRRPDLRYQLGFSVQN GIICSLMRGGIAERGGVRVGHRI IEINGQSVVATPHEKIVHILSNA VGEIHMKTMPAAMYRLL*NSS* (SEQ ID NO:316)	Eco RI / Eco RI	34MIF 5′- CGGAATTCGG AAAACTGTAA AGATG-3′ (SEQ ID NO:372) N2149-2167	20MR 5′- TCGGAATTCAG CAGCCTGTACA TCG-3′ (SEQ ID NO:373) N2690-2666
K303	KIAA0303	Ab002301	AA652-742; PDZ domain 1 (of 1) PHQPIVIHSSGKNYGFTIRAIRV YVGDSDIYTVHHIVWNVEEGSPA CQAGLKAGDLITHINGEPVHGLV HTEVIELLLKSGNKVSITTTPF*E* *FIVTD* (SEQ ID NO:317)	Bam HI / Eco RI	152KIF 5′- CTGGGATCCC ACATCAGCCG ATTGTGA-3′ (SEQ ID NO:374) N1948-1976	153KIR 5′- TGTGAATTCAA ATGGGGTAGTA GTGATTG-3′ (SEQ ID NO:375) N2237-2209

CBP	Cytohesin binding protein HE	AF68836	AA85-176; PDZ domain 1 (of 1) QRKLVTVEKQDNETFGFEIQSYR PQNQNACSSEMFTLICKIQEDSP AHCAGLQAGDVLANINGVSTEGF TYKQVVDLIRSSGNLLTIETLNG *NSS* (SEQ ID NO:318)	Bam HI / Eco RI	235CYF 5'- CCTGGATCCA AAGAAAGCTT GTTACTGTG- 3' (SEQ ID NO:376) N246-274	236CYR 5'- TCAGAATTCCA TTAAGAGTCTC TATC-3' (SEQ ID NO:377) N535-510
MINT3	human MINT3	AF029110	AA11-52; PDZ domain 1 (of 1) PVTTAIIHRPHAREQLGFCVEDG IVRPRPLAPGWGGRAALST*EFIV* *TD* (SEQ ID NO:319)	Bam HI / Eco RI	188MF 5'- ACTGGATCCC CGTCACCACC GCCATCATC- 3' (SEQ ID NO:378) N23-51	189MR 5'- CTCGAATTCCG TGCTCAGGGCC GCCCTA-3' (SEQ ID NO:379) N165-138
TAX2	human tax interaction protein 2	AF028824	AA54-140; PDZ domain 1 (of 1) RKEVEVFKSEDALGLTITDNGAG YAFIKRIKEGSVIDHIHLISVGD MIEAINGQSLLGCRHYEVARLLK ELPRGRTFTLKLTEPRK*EFIVTD* (SEQ ID NO:320)	Bam HI / Eco RI	197 TF 5'- AGGGGATCCG CAAGGAGGTG GAGGTGTTC- 3' (SEQ ID NO:380)	198 TR 5'- TGTGGAATTCC TTGCGAGGCTC CGTGAGC-3' (SEQ ID NO:381) N429-401

A4

					N154-182	
K561	KIAA0561	AB011133	AA948-1038; PDZ domain 1 (of 1) PPSLSTALARSTASACGRSASTW VIATSTLCTTSSGVWRTEAPPRR RACGLGTSSPTSTGSQCWGWCTW TSWSCCZRAATRYPCGPQPWR*IH* *RD* (SEQ ID NO:321)	Bam HI / Eco RI	161KIF 5'- CCTGGATCCC CCCATCGTTA TCCACAGC- 3' (SEQ ID NO:382) N2836-2863	162KIR 5'- GAGGAATTCTC CAGGGCTGTGG TCCG-3' (SEQ ID NO:383) N3120-3095

A6 Please replace the paragraph (TABLE 4) beginning at page 60, line 1, with the following (see attached sheets).

Please replace the paragraph beginning at page 66, line 4, with the following:

--Other investigators have reported certain PL motifs important in PDZ binding, e.g., the C-terminal motifs S/T-X-V/I/L (for DLG1) and Y/F-Y/F-I/L/F for MPP1 (see, Doyle et al., 1996, Cell 85, 1067; Songyang et al., 1997, Science 275, 73). However, the reported motifs are not sufficiently specific (i.e. a large number of proteins meet these criteria yet are not necessarily actual PDZ ligands) and cover only a small number of PDZ proteins (approximately 10). The PRISM MATRIX can be used to determine ligand specificity and to deduce ligand binding motifs for any PDZ protein because it can precisely determine sequences of amino acids that do or do not result in specific PDZ binding. In addition, the assay has revealed a significant of new PDZ domain binding motifs (i.e. PL motifs): C-terminal sequence of CD6, ISAA (SEQ ID NO:14); C- terminal sequence of

A7 CD49E, TSDA (SEQ ID NO:24); C- terminal sequence of CD49F, TSDA (SEQ ID NO:24); C-terminal sequence of CLASP-1, SAEV (SEQ ID NO:289); C- terminal sequence of CLASP-4, YAEV (SEQ ID NO:228); C- terminal sequence of CD44, KIGV (SEQ ID NO:104); C-terminal sequence of IL5R, DSVF (SEQ ID NO:94); and C-terminal sequence of BLR-1, LTTF (SEQ ID NO:253). Identification of these novel PL sequences allows the definition of novel PL motifs (See **TABLE 5A**, *infra*). The specificity with which these novel motifs are defined is enhanced by the fact that the MATRIX reports both positive results (i.e. PDZ-PL) combinations that result in specific binding interactions) and negative results (i.e. PDZ-PL combinations that do not result in specific binding). For example, the C-terminal sequence of CD6, SAA and the C-terminal sequence of CD49E, SDA bind to the PDZ-domain polypeptide 41.8 while the related C-terminal sequence of CD166, TEA and C-terminal sequence of CD148, YIA do not. This identifies the novel PL motif (Motif 1, *infra*) of polypeptides terminating in alanine with serine at the -2 position and excludes polypeptides with threonine and tyrosine at the -2 position. This motif is therefore more specific than most previously identified motifs. Other novel motifs are described in **TABLE 5A.**--

Table 4: PL Peptides

CODE	PROTEIN NAME	GENBANK ACCESS	SEQUENCE	SEQ ID NO:
AA1L	Clasp-1		ISKATPALPTVSISSSAEV	177
AA2L	Clasp-2		ISGTPTSTMVHGMTSSSSVV	178
AA3L	Clasp-4		CAISGTSSDRGYGSPRYAEV	179
AA4L	CD3n	M33158	SVFSIPTLWSPWPPSSSSQL	180
AA5L-M*	CD4	M12807	SEKKTSQSPHRFQKTCSPI	181
AA6L	CD6	X60992	SPQPDSTDNDDYDDISAA	182
AA7L	CD34	M81104	QATSRNGHSARQHVVADTEL	183
AA9L	CD44	M69215	QFMTADETRNLQNVDMKIGV	184
AA10L	CD46(Form 1)	M58050	KKGTYLTDETHREVKFTSL	185
AA11L	CD49E (4)	X06256	PYGTAMEKAQLKPPATSDA	186
AA12L	CD49F	X53586	HKAEIHAQPSDKERLTSDA	187
AA13L	CD95	M67454	KDITSDSENSNFRNEIQSLV	188
AA14L	CD97	X84700	TSGTGHNQTRALRASESGI	189
AA15L	CD98	J02939	ERLKLEPHEGLLLRFPYAA	190
AA16L	CD105	X72012	STNHSIGSTQSTPCSTSSMA	191
AA17L	VCAM1	M73255	ARKANMKGSYSLVEAQKSKV	192
AA18L	CD138	J05392	PKQANGGAYQKPTKQEEFYA	193
AA19L	CD148	D37781	ENLAPVTTFGKTNGYIA	194
AA20L	CD166	L38608	DLGNMEENKKLEENNHKTEA	195
AA22L	DNAM-1	U56102	TREDIYVNYPTFSRRPKTRV	196
AA23L-M*	FasL	U11821	SSKSKSSEESQTFFGLYKL	197
AA25L	FceRIb	D10583	YSATYSELEDPGEMSPPIDL	198
AA28L	CDW125 (IL5R)	X62156	EVICYIEKPGVETLEDSVF	199
AA29.1L	CDW128A (IL8RA)	M68932	ARHRVTSYTSSSVNVSSNL	200
AA29.2L	CDW128B (IL8RB)	M73969	KDSRPSFVGSSSGHTSTTL	201
AA30L	LPAP	X81422	AWDDSARAAGGQGLHVTAL	202
AA33L	KV1.3	AAC31761	TTNNNPNSAVNIKKIFTDV	203
AA34.2L	NMDA	NP000824	LNSCSNRRVYKKMPSIESDV	204
AA37L	Glycophorin C	AAA52574	QGDPALQDAGDSSRKEYFI	205
AA38L	Neurexin	AB011150	SSAKSSNKNKKNKDKEYYV	206
AA39L	Syndecan-2	A33880	GERKPSSAAYQKAPTKEFYA	207
AA40L	DOCK2	BAA13200	LASKSAEEGKQIPDSLSTDL	208
AA41L	CC CKR-1R	L09230	LERVSSTSPSTGEHELSAGF	209
AA42L	CC CKR-2	U03882	GKGKSIGRAPEASLQDKEGA	210
AA43L	CC CKR-3	HSU28694	LERTSSVSPSTAEPELSIVF	211
AA44L	CC CKR-4	X85740	DTPSSSYTQSTMDHDLHDAL	212
AA45L	BLR-1	S56162	PSWRRSSLSESENATSLTTF	213
AA47L	CD83	Z11697	VTSPNKHLGLVTPHKTELV	214
AA48L	CD62E	M30640	SSSQSLESDGSYQKPSYIL	215
AA49L	CD5	X04391	SMQPDNSSDSDYDLHGAQRL	216
AA55L	CD148	D37781	TIYENLAPVTTFGKTIA	217

*The Sequence studied is mutated at positions >10 amino acids from C-terminus to increase water solubility and/or eliminate intramolecular disulfides.

A6

Please replace the paragraph beginning at page 106, line 9, with the following:

--**FIGURES 3A-H** show the use of peptides to inhibit PL-PDZ interactions using the G assay described *supra*. In **FIGURE 3A and B**, the inhibiton assays were carried out using GST fusion proteins containing PDZ domains from DLG1 or PSD95 (see *supra* and **TABLE 3**). Binding of biotinylated PL peptides for CLASP-2, CD46, Fas, or KV1.3 (as listed in **TABLE 4**) was determined in the presence of various competitor peptides (at a concentration of 100 uM) or in the absence of a competitor (equalized as 100% binding). The competitor peptides were 8-mers peptides having the sequence of C-terminus of CLASP-2 (MTSSSSVV; SEQ ID NO:227), CD46 (REVKFTSL; SEQ ID NO:113), or Fas (TFFGLYKL; SEQ ID NO:83), a unlabeled
19-mer having the sequence of c-terminus of KV1.3 (i.e., non-biotinylated AA33L as listed in **TABLE 4**), or a peptide having the sequence of residues 64-76 of hemoglobin (Vidal et al., 1999, *J. Immunol.* 163, 4811), i.e., an unrelated competitor. The binding of biotinylated peptide (10 uM for Fas and KV1.3, 20 uM for CLASP-2 and CD46) to GST alone was subtracted from the binding to the fusion proteins to obtain the net signal for each experimental condition. This net signal was then normalized by dividing by the signal in the absence of competitor peptide and the data were plotted. Error bars indicated the standard deviation of duplicate measurements. Specific inhibition of CLASP-2 PL-DLG PDZ binding was observed with the CLASP-2 8-mer, the CD46
8-mer, the Fas 8-mer, and the KV1.3 peptide, but not in the absence of peptide or using an unrelated peptide.--

A8

Please replace the paragraph beginning at page 106, line 26, with the following:

--**FIGURES 3C-F** show similar assays using shorter peptides to inhibit (e.g., a 3-mer and a 5-mer). **FIGURES 3C-E** show binding of biotinylated PL peptides for CLASP-2, CD46, Fas, or KV1.3, at the indicated concentration (as listed in **TABLE 3**) to GST fusion proteins containing PDZ domains from NeDLG, DLG1, or PSD95 in the absence or presence of 1 mM 3-mer peptide having the sequence of the C-terminus of Clasp 2 (SVV) (**TABLE 3**).

A9

A9 **FIGURE 3F** shows the effect on binding of a 5-mer CD49E peptide (ATSDA; SEQ ID NO:25) to GST fusion proteins containing a PDZ domain from 41.8Kd.--

Please replace the paragraph beginning at page 109, line 3, with the following:

A10 --The C-terminal core sequence of CD49f is TSDA (SEQ ID NO:24). When naturally-occurring residues are added to the core sequence, LTSDA (SEQ ID NO:30), RLTSDA (SEQ ID NO:31), ERLTSDA (SEQ ID NO:32), and KERLTSDA (SEQ ID NO:33) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 109, line 11, with the following:

A11 --The C-terminal core sequence of CD83 is TELV (SEQ ID NO:248). When naturally-occurring residues are added to the core sequence, KTELV (SEQ ID NO:249), HKTELV (SEQ ID NO:250), PHKTELV (SEQ ID NO:251), and TPHKTELV (SEQ ID NO:252) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 110, line 21, with the following:

A12 --The C-terminal core sequence of CLASP-1 is SAQV (SEQ ID NO:218). When naturally-occurring residues are added to the core sequence, SSAQV (SEQ ID NO:219), SSSAQV (SEQ ID NO:220), ISSSAQV (SEQ ID NO:221), and SISSSAQV (SEQ ID NO:222) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 110, line 25, with the following:

A13 --The C-terminal core sequence of CLASP-2 is SSVV (SEQ ID NO:223). When naturally-occurring residues are added to the core sequence, SSSVV (SEQ ID NO:224), SSSSVV (SEQ ID NO:225), TSSSSVV (SEQ ID NO:226), and MTSSSSVV (SEQ ID NO:227) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 110, line 29, with the following:

A14

--The C-terminal core sequence of CLASP-4 is YAEV (SEQ ID NO:228). When naturally-occurring residues are added to the core sequence, RYAEV (SEQ ID NO:229), PRYAEV (SEQ ID NO:230), SPRYAEV (SEQ ID NO:231), and GSPRYAEV (SEQ ID NO:232) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 110, line 33, with the following:

A15

--The C-terminal core sequence of KV1.3 is FTDV (SEQ ID NO:238). When naturally-occurring residues are added to the core sequence, IFTDV (SEQ ID NO:239), KIFTDV (SEQ ID NO:240), KKIFTDV (SEQ ID NO:241), and IKKIFTDV (SEQ ID NO:242) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 111, line 3, with the following:

A16

--The C-terminal core sequence of DOCK2 is STDL (SEQ ID NO:243). When naturally-occurring residues are added to the core sequence, LSTDL (SEQ ID NO:244), SLSTDL (SEQ ID NO:245), DSLSTDL (SEQ ID NO:246), and PDSLSTDL (SEQ ID NO:247) may also be used to target a PDZ domain-containing protein in T cells.--

Please replace the paragraph beginning at page 111, line 22, with the following:

A17

--The C-terminal core sequence of Syndecan-2 is EFYA (SEQ ID NO:89). When naturally-occurring residues are added to the core sequence, KEFYA (SEQ ID NO:259), TKEFYA (SEQ ID NO:260), PTKEFYA (SEQ ID NO:261), and APTKEFYA (SEQ ID NO:262) may also be used to target a PDZ domain-containing protein in B cells.--

Please replace the paragraph beginning at page 111, line 26, with the following:

A18

--The C-terminal core sequence of BLR-1 is LTTF (SEQ ID NO:253). When naturally-occurring residues are added to the core sequence, SLTTF (SEQ ID NO:254), TSLTTF (SEQ ID NO:255), ATSLTTF (SEQ ID NO:256), and NATSLTTF (SEQ ID NO:257) may also be used to target a PDZ domain-containing protein in B cells.--

Please replace the paragraph beginning at page 114, line 5, with the following:

A19

--The C-terminal core sequence of CD105 is SSMA (SEQ ID NO:159). When naturally-occurring residues are added to the core sequence, TSSMA (SEQ ID NO:160), STSSMA (SEQ ID NO:161), CSTSSMA (SEQ ID NO:291) and PCSTSSMA (SEQ ID NO:162) may also be used to target a PDZ domain-containing protein in endothelial cells.--

Please replace the paragraph beginning at page 114, line 17, with the following:

A20

--The C-terminal core sequence of VCAM1 is KSKV (SEQ ID NO:163). When naturally-occurring residues are added to the core sequence, QKSKV (SEQ ID NO:164), AQKSKV (SEQ ID NO:165), EAQKSKV (SEQ ID NO:166), and VEAQKSKV (SEQ ID NO:167) may also be used to target a PDZ domain-containing protein in endothelial cells.--

Please replace the paragraph beginning at page 114, line 23, with the following:

A21

--FcεRIβ, CDw125, CDw128 and IL-8RB are transmembrane receptors expressed by mast cells, basophils and eosinophils. These receptors play a role in the activation of these cells to result in degranulation and histamine release in allergic reactions. The C-terminal core sequence of FcεRIβ is PIDL (SEQ ID NO:129). When naturally-occurring residues are added to the core sequence, PPIDL (SEQ ID NO:130), SPPIDL (SEQ ID NO:131), MSPPIDL (SEQ ID NO:132) and EMSPPIDL (SEQ ID NO:133) may also be used to target a PDZ domain-containing protein in mast cells. In addition, the residue E may be substituted with G to increase its binding affinity.--

Please replace the paragraph beginning at page 114, line 31, with the following:

A22

--The C-terminal core sequence of CDw125 is DSVF (SEQ ID NO:94). When naturally-occurring residues are added to the core sequence, EDSVF (SEQ ID NO:95), LEDSVF (SEQ ID NO:96), TLEDSVF (SEQ ID NO:97), and ETLEDSVF (SEQ ID NO:98) may also be used to target a PDZ domain-containing protein in mast cells.--

Please replace the paragraph beginning at page 115, line 1, with the following:

A23

--The C-terminal core sequence of CDw128 is SSNL (SEQ ID NO:69). When naturally-occurring residues are added to the core sequence, VSSNL (SEQ ID NO:70), NVSSNL (SEQ ID NO:71), VNVSSNL (SEQ ID NO:72), and SVNVSSNL (SEQ ID NO:73) may also be used to target a PDZ domain-containing protein in mast cells.--

Please replace the paragraph beginning at page 115, line 5, with the following:

A24

--The C-terminal core sequence of IL-8RB is STTL (SEQ ID NO:233). When naturally-occurring residues are added to the core sequence TSTTL (SEQ ID NO:234), HTSTTL (SEQ ID NO:235), GHTSTTL (SEQ ID NO:236) and SGHTSTTL (SEQ ID NO:237) may also be used to target a PDZ domain-containing protein in mast cells.--

Please replace the paragraph beginning at page 115, line 10, with the following:

A25

--The C-terminal core sequence of NMDA is ESDV (SEQ ID NO:263). When naturally-occurring residues are added to the core sequence, IESDV (SEQ ID NO:264), SIESDV (SEQ ID NO:265), PSIESDV (SEQ ID NO:266), and MPSIESDV (SEQ ID NO:267) may also be used to target a PDZ domain-containing protein in neuronal cells.--

Please replace the paragraph beginning at page 115, line 14, with the following:

--The C-terminal core sequence of neurexin is EYYV (SEQ ID NO:268). When naturally-occurring residues are added to the core sequence, KEYYV (SEQ ID NO:269), DKEYYV (SEQ ID NO:270), KDKEYYV (SEQ ID NO:271), and NKDKEYYV (SEQ ID NO:272) may also be used to target a PDZ domain-containing protein in neuronal cells.--

A26

Please replace the paragraph beginning at page 115, line 19, with the following:

--The C-terminal core sequence of Glycophorin C is EYFI (SEQ ID NO:273). When naturally-occurring residues are added to the core sequence, KEYFI (SEQ ID NO:274), RKEYFI (SEQ ID NO:275), SRKEYFI (SEQ ID NO:276), and SSRKEYFI (SEQ ID NO:277) may also be used to target a PDZ domain-containing protein.--

A27

Please replace the paragraph beginning at page 115, line 23, with the following:

--The C-terminal core sequence of CD148 is KTIA (SEQ ID NO:278). When naturally-occurring residues are added to the core sequence, GKTIA (SEQ ID NO:279), FGKTIA (SEQ ID NO:280), TFGKTIA (SEQ ID NO:281), and TTFGKTIA (SEQ ID NO:282) may also be used to target a PDZ domain-containing protein in epithelial or myeloid cells.--

A28

Please replace the paragraph beginning at page 138, line 9, with the following:

--All peptides were chemically synthesized by standard procedures. The Tat-CD3 carboxyl terminus fusion peptide, (GYGRKKRRQRRRGPPSSSSGL, SEQ ID NO:174); Tat-CLASP1 carboxyl terminus fusion peptide, (GYGRKKRRQRRRGSISSSAEV, SEQ ID NO:175); Tat-CLASP2 carboxyl terminus fusion peptide, (GYGRKKRRQRRRGMTSSSSVV, SEQ ID NO:176); and Tat peptide, (GYGRKKRRQRRRG, SEQ ID NO:289); were dissolved at 1 mM in PBS, pH 7, or dH2O. Stock MBPAc1-16 peptide, (AcASQKRPSQRHGSKYLA; SEQ ID NO:290), was dissolved at 5 mM. All peptides were aliquoted and stored at -80^0C until tested.--

A29

Please replace the paragraph beginning at page 140, line 24, with the following:

--To detect such inhibition, it was necessary to synthesize an analogue of the CLASP2peptide AA2L that (1) retained similar DLG1 binding properties and (2) would not itself generate a signal in the assay selected to measure inhibition. Because most molecular interactions between PDZ proteins and their ligands involve only the C-terminal 6 amino acids of the ligand, an eight amino acid variant of the CLASP-2 peptide, MTSSSSVV (SEQ ID NO:227), was anticipated to retain similar DLG1 binding properties as the 20 amino acid AA2L CLASP-2 peptide. This eight amino acid CLASP-2 peptide (lacking a functional label) was therefore synthesized and purified by standard techniques as described *supra*. When 100 uM of the (functionally unlabeled) eight amino acid CLASP-2 peptide and 20 uM of the biotin-labeled AA2L CLASP-2 peptide were added simultaneously to DLG1 in a variant of the "G" assay (described supra), the binding of the labeled AA2L CLASP-2 peptide was, as predicted, inhibited by greater than 50% (**FIGURE 3A**). An analogous experiment in which the labeled AA2L CLASP-2 peptide was replaced with another labeled DLG1 ligand, labeled AAI3L Fas peptide demonstrated similar inhibition by the eight amino acid CLASP-2 peptide (**FIGURE 3A**). Thus, an effective inhibitor of DLG1-ligand binding (i.e. the eight amino acid CLASP-2 peptide MTSSSSVV; SEQ ID NO:227) with a known potency range (order of magnitude 21 uM) was designed based on knowledge of the affinity, 21 uM, with which a particular labeled ligand, the CLASP-2 peptide AA2L, bound to DLG1.--

A30

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 88, at the end of the application.

REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-383, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.